



A; Molecule type: mRNA  
 A; Residues 'F, 212-213, 223-860 <HI2>  
 A; Cross-references: DDBJ:AB00176; NID:92605478; PID:92605479  
 A; Experimental source: PC-12 cell  
 C; Comment: This Protein is a member of the epidermal growth factor family. It is functionalizing the differentiation of MDA-MB-453 cells.  
 C; Superfamily: human ErbB kinase activator alpha, brain and thymus; EGR homology; immunoglobulin-like domain; Ig-like #status predicted <IGL>  
 C; Keywords: glycoprotein  
 F; 361-397/Domain: Ig-like #status predicted <IGL>  
 F; 422-444/Domain: hydrophobic #status predicted <HWD>  
 F; 163-294-467/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 47.4%; Score 9; DB 2; Length 860;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EARARRAA 10  
 Db 570 EARARRAA 578

RESULT 3  
 JC5701  
 Erbb kinase activator alpha1, brain and thymus - rat  
 C; Species: Rattus norvegicus (Norway rat)  
 C; Date: 25-Nov-1997 #sequence\_revision 25-Nov-1997 #text\_change 08-Sep-2002  
 C; Accession: JC5701; PC411  
 F; Miyashita, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakagawa, T.; Miyagawa, H.; Biochem 122, 675-680, 1997  
 A; Title: A novel brain-derived member of the epidermal growth factor family that interacts with the human ErbB kinase activator alpha1  
 A; Reference number: JC5700; PMID:98006324; PMID:9348101  
 A; Accession: JC5701  
 A; Molecule type: mRNA  
 A; Residues 1-868 <HIG>  
 A; Cross-references: DDBJ:D89995; NID:92605629; PID:92605630  
 A; Accession: PC411  
 A; Molecule type: protein  
 A; Residues 128-162 <HI2>  
 A; Experimental source: PC-12 cell  
 C; Comment: This Protein is a member of the epidermal growth factor family. It is functionalizing the differentiation of MDA-MB-453 cells.  
 C; Superfamily: human ErbB kinase activator alpha, brain and thymus; EGR homology; immunoglobulin-like domain; EGR homology <EGF>  
 Query Match 47.4%; Score 9; DB 2; Length 860;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EARARRAA 10  
 Db 578 EARARRAA 586

RESULT 4  
 H72702  
 hypothetical protein APE1039 - Aeropyrum pernix (strain K1)  
 C; Species: Aeropyrum pernix  
 C; Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C; Accession: H72702  
 R; Kavarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-91, 1999  
 A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum  
 A; Accession number: A72450; PMID:99310339; PMID:10382966  
 A; Status: Preliminary  
 A; Molecule type: DNA  
 A; Residues 1-144 <RAW>  
 A; Cross-references: DDBJ:AP000060; NID:95104188; PID:92605479; PID:951043810; PID:951043811  
 C; Genomics: Sinorhizobium meliloti (strain 1021) magaplasmid pSTM  
 A; Gene: APP1039

RESULT 5  
 T34685  
 ABC-transporter ATP-binding protein - Streptomyces coelicolor  
 C; Species: Streptomyces coelicolor  
 C; Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 17-Mar-2000  
 C; Accession: T34685  
 R; Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 A; Reference number: 221553  
 A; Accession: T34685  
 A; Status: Preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues 1-264 <HAR>  
 A; Cross-references: EMBL:AL023517; PRDN:CAA18981.1; GSPDB:GN00070; SCOEDB:SC1B5.07

C; Genetics:  
 A; Experimental source: strain A3(2)  
 C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog  
 Query Match 42.1%; Score 8; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 RRAARRAA 13  
 Db 99 RRAARRAA 106

RESULT 6  
 H83363  
 pyoverdine biosynthesis protein Pvca PA2254 [Imported] - Pseudomonas aeruginosa (strain PAO1)  
 C; Species: Pseudomonas aeruginosa  
 C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C; Accession: H83363  
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000  
 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A; Reference Number: 82950; MUID:20437337; PMID:10984043  
 A; Status: Preliminary  
 A; Molecule type: DNA  
 A; Residues 1-348 <SP0>  
 A; Cross-references: GB:AE004651; GB:AE004091; NID:99948277; PIDN:AAG05642.1; GSPDB:GN  
 C; Genetics:  
 A; Gene: Pvca; PA2254

Query Match 42.1%; Score 8; DB 2; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 ARARRAA 17  
 Db 319 ARARRAA 326

RESULT 7  
 E95279  
 probable [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSTM  
 C; Species: Sinorhizobium meliloti  
 C; Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C;Accession: E95279  
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
 R;Kelman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*  
 A;Reference number: A95262, MUID:21396509, PMID:11481432  
 A;Accession: E95279  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-334 <KDR>  
 A;Cross-references: GB:AE006459; PIDN:AK64799.1; PID:g14523209; GSPDB:GN00165  
 A;Experimental source: strain 1021, megaplasmid pSma  
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hynes, R.W.; Jones, T.  
 Science 293, 688-692, 2001  
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leaure,  
 Hebbault, P.; Vandenkoornhuyse, M.; Verholtshaar, F.J.; Weidner, S.; Wells, D.H.; Yeh, K.  
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A;Content: number: A96039; MUID:21368234; PMID:11474104  
 A;Content: annotation  
 C;Genetics:  
 A;Gene: Sha0265  
 C;Superfamily: malate dehydrogenase Ylbc  
 Query Match 42.1%; Score 8; DB 2; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 ARARRAA 10  
 |||||  
 Db 306 ARARRAA 313  
 .  
 RESULT 8  
 KISMG  
 galactokinase (EC 2.7.1.6) - *Streptomyces* sp.  
 C;Species: *Streptomyces* sp.  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 28-May-1999  
 C;Accession: C28669  
 R;Adams, C.W.; Fornwald, J.A.; Schmidt, F.J.; Rosenberg, M.; Brawner, M.E.  
 A;Title: Gene organization and structure of the *Streptomyces lividans* gal operon.  
 A;Reference number: A28669; MUID:88086869; PMID:3335481  
 A;Accession: C28669  
 A;Molecule type: DNA  
 A;Residues: 1-395 <ADA>  
 A;Cross-references: GB:MI8953; NID:153259; PIDN:AAA26748.1; PID:g153262  
 C;Genetics:  
 A;Gene: galK  
 C;Superfamily: galactokinase  
 C;Keywords: ATP; galactokinase metabolism; phosphotransferase  
 Query Match 42.1%; Score 8; DB 1; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 AARAARRA 16  
 |||||  
 Db 228 AARAARRA 235  
 .  
 RESULT 9  
 T34741  
 hypothetical protein SC1E6\_20c SC1E6\_20c - *Streptomyces coelicolor*  
 C;Species: *Streptomyces coelicolor*  
 C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
 C;Accession: T34741  
 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 A;Reference number: Z21555  
 A;Content: reference to the EMBL Data Library, November 1998

A; Accession: T34741  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 1-501 <SEE>  
A; Cross-references: EMLN:AL033505; PIDN:CAA22048.1; GSPDB:GN00070; SCOEDB:SC1E6.20c  
A; Experimental source: strain A312  
A; Genetics:  
A; Gene: SCOEDB:SC1E6.20c

Matches	8	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	4	RARRAAR 11							
Db	249	RARRAAR 256							
<b>RESULT 12</b>									
G8072	hypothetical protein BH3383 [Imported] - <i>Bacillus halodurans</i> (strain C-125)								
C:Species	<i>Bacillus halodurans</i>								
C:Accession	G84072								
C:Title	Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and								
A:Reference Number	A83650; PMID:11058132								
A:Accession	G84072								
A:Status	Preliminary								
A:Molecule type	DNA								
A:Residues	1-57 <STO>								
A:Cross-references	GB:AP001518; NID:BA0000004; PMID:910175792; PIDN:q10175792; PIDN:BA007102.1; GSPDB:GN000								
A:Experimental source	strain C-125								
C:Genetics									
A:Gene	BH3383								
Query Match	36.8%	Score 7;	DB 2;	Length 57;					
Best Local Similarity	100.0%	Pred. No. 11;							
Matches	7	Conservative	0;	Mismatches	0;	Indels	0	Gaps	0;
Qy	8	AARRAAR 14							
Db	27	ARRAARR 33							
<b>RESULT 13</b>									
A13052	hypothetical protein Atu4038 [Imported] - <i>Agrobacterium tumefaciens</i> (strain C58, Dupont)								
C:Species	<i>Agrobacterium tumefaciens</i>								
C:Accession	A13052								
C:Title	Complete genome sequence revision 11-Jan-2002 #text_change 18-Nov-2002								
R:Wood	D. W.	Surabhi, J. C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G. E.; Chen, Y.; Woo, I.; George, G.; Gillett, W.; Grant, C.; Guenther, D.; Levy, R.; Li, M.; McClelland, J.; Karp, P.; Romero, P.; Zhang, S.							
R:Authors	Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.W.								
A:Title	The Genome of the Natural Genetic Engineer <i>Agrobacterium tumefaciens</i> C58.								
A:Accession	A13052								
A:Status	Preliminary								
A:Molecule type	DNA								
A:Residues	1-71 <STO>								
Query Match	36.8%	Score 7;	DB 2;	Length 126;					
Best Local Similarity	100.0%	Pred. No. 21;							
Matches	7	Conservative	0;	Mismatches	0;	Indels	0	Gaps	0;
Qy	7	RAAAARRA 13							
Db	105	RAAAARRA 111							

RESULT 14  
A87663 hypothetical protein CC3339 [imported] - *Caulobacter crescentus*  
C:Species: *Caulobacter crescentus*  
C:Date: 20-Apr-2001 \*sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001